



**Biotechnology Systems Branch**

**RAW SEQUENCE LISTING**  
**ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/575,096  
Source: IFWP  
Date Processed by STIC: 4/24/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER** **VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):  
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

## Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	SERIAL NUMBER: <u>10/575,096</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 <u>Wrapped Nucleics</u> <u>Wrapped Aminos</u>	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <u>Invalid Line Length</u>	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <u>Misaligned Amino Numbering</u>	The numbering under each 5 <sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 <u>Non-ASCII</u>	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 <u>Variable Length</u>	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 <u>PatentIn 2.0 "bug"</u>	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 <u>Skipped Sequences (OLD RULES)</u>	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped  Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 <u>Skipped Sequences (NEW RULES)</u>	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 <u>Use of n's or Xaa's (NEW RULES)</u>	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 <u>Invalid &lt;213&gt; Response</u>	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 <u>Use of &lt;220&gt;</u>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 <u>PatentIn 2.0 "bug"</u>	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 <u>Misuse of n/Xaa</u>	"n" can only represent a single <u>nucleotide</u> ; "Xaa" can only represent a single <u>amino acid</u>	



IFWP

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/575,096

DATE: 04/24/2006  
TIME: 16:09:54

Input Set : A:\PTO.KD.txt  
Output Set: N:\CRF4\04242006\J575096.raw

*see item 2 on  
✓ Enn summary  
sheet*

3 <110> APPLICANT: KYOWA HAKKO KOGYO CO., LTD.  
5 <120> TITLE OF INVENTION: Process for the antibody composition using RNA  
which inhibits a function  
6 of a1,6-fucosyltransferase  
8 <130> FILE REFERENCE: 11621WO1  
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/575,096  
C--> 10 <141> CURRENT FILING DATE: 2006-04-10  
10 <150> PRIOR APPLICATION NUMBER: P2003-350167  
11 <151> PRIOR FILING DATE: 2003-10-09  
E--> 13 <160> NUMBER OF SEQ ID NOS: 35 (p.10)  
15 <170> SOFTWARE: PatentIn Ver. 2.1

*pp 1-246-10*

## ERRORED SEQUENCES

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268 <212> TYPE: PRT  
269 <213> ORGANISM: Cricetulus griseus  
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275 Ala Trp Gly Thr Leu Leu Phe Tyr Ile Gly Gly His Leu Val Arg Asp  
276 20 25 30  
278 Asn Asp His Pro Asp His Ser Ser Arg Glu Leu Ser Lys Ile Leu Ala  
279 35 40 45  
281 Lys Leu Glu Arg Leu Lys Gln Gln Asn Glu Asp Leu Arg Arg Met Ala  
282 50 55 60  
284 Glu Ser Leu Arg Ile Pro Glu Gly Pro Ile Asp Gln Gly Thr Ala Thr  
285 65 70 75 80  
287 Gly Arg Val Arg Val Leu Glu Glu Gln Leu Val Lys Ala Lys Glu Gln  
288 85 90 95  
290 Ile Glu Asn Tyr Lys Lys Gln Ala Arg Asn Asp Leu Gly Lys Asp His  
291 100 105 110  
293 Glu Ile Leu Arg Arg Arg Ile Glu Asn Gly Ala Lys Glu Leu Trp Phe  
294 115 120 125  
296 Phe Leu Gln Ser Glu Leu Lys Lys Leu Lys Lys Leu Glu Gly Asn Glu  
297 130 135 140  
299 Leu Gln Arg His Ala Asp Glu Ile Leu Leu Asp Leu Gly His His Glu  
300 145 150 155 160  
302 Arg Ser Ile Met Thr Asp Leu Tyr Tyr Leu Ser Gln Thr Asp Gly Ala  
303 165 170 175  
305 Gly Glu Trp Arg Glu Lys Glu Ala Lys Asp Leu Thr Glu Leu Val Gln  
306 180 185 190

*p.2*  
**Does Not Comply  
Corrected Diskette Needed**

## RAW SEQUENCE LISTING

DATE: 04/24/2006

PATENT APPLICATION: US/10/575,096

TIME: 16:09:54

Input Set : A:\PTO.KD.txt

Output Set: N:\CRF4\04242006\J575096.raw

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308 Arg Arg Ile Thr Tyr Leu Gln Asn Pro Lys Asp Cys Ser Lys Ala Arg
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311 Lys Leu Val Cys Asn Ile Asn Lys Gly Cys Gly Tyr Gly Cys Gln Leu
312      210      215      220
314 His His Val Val Tyr Cys Phe Met Ile Ala Tyr Gly Thr Gln Arg Thr
315 225      230      235      240
317 Leu Ile Leu Glu Ser Gln Asn Trp Arg Tyr Ala Thr Gly Gly Trp Glu
318      245      250      255
320 Thr Val Phe Arg Pro Val Ser Glu Thr Cys Thr Asp Arg Ser Gly Leu
321      260      265      270
323 Ser Thr Gly His Trp Ser Gly Glu Val Lys Asp Lys Asn Val Gln Val
324      275      280      285
326 Val Glu Leu Pro Ile Val Asp Ser Leu His Pro Arg Pro Pro Tyr Leu
327      290      295      300
329 Pro Leu Ala Val Pro Glu Asp Leu Ala Asp Arg Leu Leu Arg Val His
330 305      310      315      320
332 Gly Asp Pro Ala Val Trp Trp Val Ser Gln Phe Val Lys Tyr Leu Ile
333      325      330      335
335 Arg Pro Gln Pro Trp Leu Glu Arg Glu Ile Glu Glu Thr Thr Lys Lys
336      340      345      350
338 Leu Gly Phe Lys His Pro Val Ile Gly Val His Val Arg Arg Thr Asp
339      355      360      365
341 Lys Val Gly Thr Glu Ala Ala Phe His Pro Ile Glu Glu Tyr Met Val
342      370      375      380
344 His Val Glu Glu His Phe Gln Leu Leu Glu Arg Arg Met Lys Val Asp
345 385      390      395      400
347 Lys Lys Arg Val Tyr Leu Ala Thr Asp Asp Pro Ser Leu Leu Lys Glu
348      405      410      415
350 Ala Lys Thr Lys Tyr Ser Asn Tyr Glu Phe Ile Ser Asp Asn Ser Ile
351      420      425      430
353 Ser Trp Ser Ala Gly Leu His Asn Arg Tyr Thr Glu Asn Ser Leu Arg
354      435      440      445
356 Gly Val Ile Leu Asp Ile His Phe Leu Ser Gln Ala Asp Phe Leu Val
357      450      455      460
359 Cys Thr Phe Ser Ser Gln Val Cys Arg Val Ala Tyr Glu Ile Met Gln
360 465      470      475      480
362 Thr Leu His Pro Asp Ala Ser Ala Asn Phe His Ser Leu Asp Asp Ile
363      485      490      495
365 Tyr Tyr Phe Gly Gly Gln Asn Ala His Asn Gln Ile Ala Val Tyr Pro
366      500      505      510
368 His Gln Pro Arg Thr Lys Glu Glu Ile Pro Met Glu Pro Gly Asp Ile
369      515      520      525
371 Ile Gly Val Ala Gly Asn His Trp Asn Gly Tyr Ser Lys Gly Val Asn
372      530      535      540
374 Arg Lys Leu Gly Lys Thr Gly Leu Tyr Pro Ser Tyr Lys Val Arg Glu
375 545      550      555      560
377 Lys Ile Glu Thr Val Lys Tyr Pro Thr Tyr Pro Glu Ala Glu Lys
E--> 378      565      570
381 <210> SEQ ID NO: 6

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578 ← insert

P.4

## RAW SEQUENCE LISTING

DATE: 04/24/2006

PATENT APPLICATION: US/10/575,096

TIME: 16:09:54

Input Set : A:\PTO.KD.txt

Output Set: N:\CRF4\04242006\J575096.raw

382 &lt;211&gt; LENGTH: 575

383 &lt;212&gt; TYPE: PRT

384 &lt;213&gt; ORGANISM: Mus musculus

386 &lt;400&gt; SEQUENCE: 6

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391           20           25           30
393 Asn Asp His Pro Asp His Ser Ser Arg Glu Leu Ser Lys Ile Leu Ala
394           35           40           45
396 Lys Leu Glu Arg Leu Lys Gln Gln Asn Glu Asp Leu Arg Arg Met Ala
397           50           55           60
399 Glu Ser Leu Arg Ile Pro Glu Gly Pro Ile Asp Gln Gly Thr Ala Thr
400   65           70           75           80
402 Gly Arg Val Arg Val Leu Glu Glu Gln Leu Val Lys Ala Lys Glu Gln
403           85           90           95
405 Ile Glu Asn Tyr Lys Lys Gln Ala Arg Asn Gly Leu Gly Lys Asp His
406           100          105          110
408 Glu Ile Leu Arg Arg Arg Ile Glu Asn Gly Ala Lys Glu Leu Trp Phe
409           115          120          125
411 Phe Leu Gln Ser Glu Leu Lys Lys Leu Lys His Leu Glu Gly Asn Glu
412           130          135          140
414 Leu Gln Arg His Ala Asp Glu Ile Leu Leu Asp Leu Gly His His Glu
415 145           150          155          160
417 Arg Ser Ile Met Thr Asp Leu Tyr Tyr Leu Ser Gln Thr Asp Gly Ala
418           165          170          175
420 Gly Asp Trp Arg Glu Lys Glu Ala Lys Asp Leu Thr Glu Leu Val Gln
421           180          185          190
423 Arg Arg Ile Thr Tyr Leu Gln Asn Pro Lys Asp Cys Ser Lys Ala Arg
424           195          200          205
426 Lys Leu Val Cys Asn Ile Asn Lys Gly Cys Gly Tyr Gly Cys Gln Leu
427           210          215          220
429 His His Val Val Tyr Cys Phe Met Ile Ala Tyr Gly Thr Gln Arg Thr
430 225           230          235          240
432 Leu Ile Leu Glu Ser Gln Asn Trp Arg Tyr Ala Thr Gly Gly Trp Glu
433           245          250          255
435 Thr Val Phe Arg Pro Val Ser Glu Thr Cys Thr Asp Arg Ser Gly Leu
436           260          265          270
438 Ser Thr Gly His Trp Ser Gly Glu Val Asn Asp Lys Asn Ile Gln Val
439           275          280          285
441 Val Glu Leu Pro Ile Val Asp Ser Leu His Pro Arg Pro Pro Tyr Leu
442           290          295          300
444 Pro Leu Ala Val Pro Glu Asp Leu Ala Asp Arg Leu Leu Arg Val His
445 305           310          315          320
447 Gly Asp Pro Ala Val Trp Trp Val Ser Gln Phe Val Lys Tyr Leu Ile
448           325          330          335
450 Arg Pro Gln Pro Trp Leu Glu Lys Glu Ile Glu Glu Ala Thr Lys Lys
451           340          345          350
453 Leu Gly Phe Lys His Pro Val Ile Gly Val His Val Arg Arg Thr Asp

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DATE: 04/24/2006

TIME: 16:09:54

Input Set : A:\PTO.KD.txt

Output Set: N:\CRF4\04242006\J575096.raw

454 355 360 365  
 456 Lys Val Gly Thr Glu Ala Ala Phe His Pro Ile Glu Glu Tyr Met Val  
 457 370 375 380  
 459 His Val Glu Glu His Phe Gln Leu Leu Ala Arg Arg Met Gln Val Asp  
 460 385 390 395 400  
 462 Lys Lys Arg Val Tyr Leu Ala Thr Asp Asp Pro Thr Leu Leu Lys Glu  
 463 405 410 415  
 465 Ala Lys Thr Lys Tyr Ser Asn Tyr Glu Phe Ile Ser Asp Asn Ser Ile  
 466 420 425 430  
 468 Ser Trp Ser Ala Gly Leu His Asn Arg Tyr Thr Glu Asn Ser Leu Arg  
 469 435 440 445  
 471 Gly Val Ile Leu Asp Ile His Phe Leu Ser Gln Ala Asp Phe Leu Val  
 472 450 455 460  
 474 Cys Thr Phe Ser Ser Gln Val Cys Arg Val Ala Tyr Glu Ile Met Gln  
 475 465 470 475 480  
 477 Thr Leu His Pro Asp Ala Ser Ala Asn Phe His Ser Leu Asp Asp Ile  
 478 485 490 495  
 480 Tyr Tyr Phe Gly Gly Gln Asn Ala His Asn Gln Ile Ala Val Tyr Pro  
 481 500 505 510  
 483 His Lys Pro Arg Thr Glu Glu Glu Ile Pro Met Glu Pro Gly Asp Ile  
 484 515 520 525  
 486 Ile Gly Val Ala Gly Asn His Trp Asp Gly Tyr Ser Lys Gly Ile Asn  
 487 530 535 540  
 489 Arg Lys Leu Gly Lys Thr Gly Leu Tyr Pro Ser Tyr Lys Val Arg Glu  
 490 545 550 555 560  
 492 Lys Ile Glu Thr Val Lys Tyr Pro Thr Tyr Pro Glu Ala Glu Lys  
 493 565 570  
 496 <210> SEQ ID NO: 7  
 497 <211> LENGTH: 575  
 498 <212> TYPE: PRT  
 E--> 499 <214> Rattus norvegicus  
 501 <400> SEQUENCE: 7  
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 503 1 5 10 15  
 505 Ala Trp Gly Thr Leu Leu Phe Tyr Ile Gly Gly His Leu Val Arg Asp  
 506 20 25 30  
 508 Asn Asp His Pro Asp His Ser Ser Arg Glu Leu Ser Lys Ile Leu Ala  
 509 35 40 45  
 511 Lys Leu Glu Arg Leu Lys Gln Gln Asn Glu Asp Leu Arg Arg Met Ala  
 512 50 55 60  
 514 Glu Ser Leu Arg Ile Pro Glu Gly Pro Ile Asp Gln Gly Thr Ala Thr  
 515 65 70 75 80  
 517 Gly Arg Val Arg Val Leu Glu Glu Gln Leu Val Lys Ala Lys Glu Gln  
 518 85 90 95  
 520 Ile Glu Asn Tyr Lys Lys Gln Ala Arg Asn Gly Leu Gly Lys Asp His  
 521 100 105 110  
 523 Glu Ile Leu Arg Arg Arg Ile Glu Asn Gly Ala Lys Glu Leu Trp Phe  
 524 115 120 125

575 ← insert

see p. 6

## RAW SEQUENCE LISTING

DATE: 04/24/2006

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TIME: 16:09:54

Input Set : A:\PTO.KD.txt

Output Set: N:\CRF4\04242006\J575096.raw

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526 Phe Leu Gln Ser Glu Leu Lys Lys Leu Lys His Leu Glu Gly Asn Glu
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529 Leu Gln Arg His Ala Asp Glu Ile Leu Leu Asp Leu Gly His His Glu
530 145      150      155      160
532 Arg Ser Ile Met Thr Asp Leu Tyr Tyr Leu Ser Gln Thr Asp Gly Ala
533      165      170      175
535 Gly Asp Trp Arg Glu Lys Glu Ala Lys Asp Leu Thr Glu Leu Val Gln
536      180      185      190
538 Arg Arg Ile Thr Tyr Leu Gln Asn Pro Lys Asp Cys Ser Lys Ala Arg
539      195      200      205
541 Lys Leu Val Cys Asn Ile Asn Lys Gly Cys Gly Tyr Gly Cys Gln Leu
542      210      215      220
544 His His Val Val Tyr Cys Phe Met Ile Ala Tyr Gly Thr Gln Arg Thr
545 225      230      235      240
547 Leu Ile Leu Glu Ser Gln Asn Trp Arg Tyr Ala Thr Gly Gly Trp Glu
548      245      250      255
550 Thr Val Phe Arg Pro Val Ser Glu Thr Cys Thr Asp Arg Ser Gly Leu
551      260      265      270
553 Ser Thr Gly His Trp Ser Gly Glu Val Asn Asp Lys Asn Ile Gln Val
554      275      280      285
556 Val Glu Leu Pro Ile Val Asp Ser Leu His Pro Arg Pro Pro Tyr Leu
557      290      295      300
559 Pro Leu Ala Val Pro Glu Asp Leu Ala Asp Arg Leu Val Arg Val His
560 305      310      315      320
562 Gly Asp Pro Ala Val Trp Trp Val Ser Gln Phe Val Lys Tyr Leu Ile
563      325      330      335
565 Arg Pro Gln Pro Trp Leu Glu Lys Glu Ile Glu Glu Ala Thr Lys Lys
566      340      345      350
568 Leu Gly Phe Lys His Pro Val Ile Gly Val His Val Arg Arg Thr Asp
569      355      360      365
571 Lys Val Gly Thr Glu Ala Ala Phe His Pro Ile Glu Glu Tyr Met Val
572      370      375      380
574 His Val Glu Glu His Phe Gln Leu Leu Ala Arg Arg Met Gln Val Asp
575 385      390      395      400
577 Lys Lys Arg Val Tyr Leu Ala Thr Asp Asp Pro Ala Leu Leu Lys Glu
578      405      410      415
580 Ala Lys Thr Lys Tyr Ser Asn Tyr Glu Phe Ile Ser Asp Asn Ser Ile
581      420      425      430
583 Ser Trp Ser Ala Gly Leu His Asn Arg Tyr Thr Glu Asn Ser Leu Arg
584      435      440      445
586 Gly Val Ile Leu Asp Ile His Phe Leu Ser Gln Ala Asp Phe Leu Val
587      450      455      460
589 Cys Thr Phe Ser Ser Gln Val Cys Arg Val Ala Tyr Glu Ile Met Gln
590 465      470      475      480
592 Thr Leu His Pro Asp Ala Ser Ala Asn Phe His Ser Leu Asp Asp Ile
593      485      490      495
595 Tyr Tyr Phe Gly Gly Gln Asn Ala His Asn Gln Ile Ala Val Tyr Pro
596      500      505      510
598 His Lys Pro Arg Thr Asp Glu Glu Ile Pro Met Glu Pro Gly Asp Ile

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## RAW SEQUENCE LISTING

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TIME: 16:09:54

Input Set : A:\PTO.KD.txt

Output Set: N:\CRF4\04242006\J575096.raw

599                    515                    520                    525  
 601 Ile Gly Val Ala Gly Asn His Trp Asp Gly Tyr Ser Lys Gly Val Asn  
 602                    530                    535                    540  
 604 Arg Lys Leu Gly Lys Thr Gly Leu Tyr Pro Ser Tyr Lys Val Arg Glu  
 605 545                    550                    555                    560  
 607 Lys Ile Glu Thr Val Lys Tyr Pro Thr Tyr Pro Glu Ala Glu Lys  
 E--> 608                    565                    570                    575 ← insert  
 611 <210> SEQ ID NO: 8  
 612 <211> LENGTH: 575  
 613 <212> TYPE: PRT  
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 618 1                    5                    10                    15  
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 621                    20                    25                    30  
 623 Asn Asp His Pro Asp His Ser Ser Arg Glu Leu Ser Lys Ile Leu Ala  
 624                    35                    40                    45  
 626 Lys Leu Glu Arg Leu Lys Gln Gln Asn Glu Asp Leu Arg Arg Met Ala  
 627                    50                    55                    60  
 629 Glu Ser Leu Arg Ile Pro Glu Gly Pro Ile Asp Gln Gly Pro Ala Ile  
 630 65                    70                    75                    80  
 632 Gly Arg Val Arg Val Leu Glu Glu Gln Leu Val Lys Ala Lys Glu Gln  
 633                    85                    90                    95  
 635 Ile Glu Asn Tyr Lys Lys Gln Thr Arg Asn Gly Leu Gly Lys Asp His  
 636                    100                    105                    110  
 638 Glu Ile Leu Arg Arg Arg Ile Glu Asn Gly Ala Lys Glu Leu Trp Phe  
 639                    115                    120                    125  
 641 Phe Leu Gln Ser Glu Leu Lys Lys Leu Lys Asn Leu Glu Gly Asn Glu  
 642                    130                    135                    140  
 644 Leu Gln Arg His Ala Asp Glu Phe Leu Leu Asp Leu Gly His His Glu  
 645 145                    150                    155                    160  
 647 Arg Ser Ile Met Thr Asp Leu Tyr Tyr Leu Ser Gln Thr Asp Gly Ala  
 648                    165                    170                    175  
 650 Gly Asp Trp Arg Glu Lys Glu Ala Lys Asp Leu Thr Glu Leu Val Gln  
 651                    180                    185                    190  
 653 Arg Arg Ile Thr Tyr Leu Gln Asn Pro Lys Asp Cys Ser Lys Ala Lys  
 654                    195                    200                    205  
 656 Lys Leu Val Cys Asn Ile Asn Lys Gly Cys Gly Tyr Gly Cys Gln Leu  
 657                    210                    215                    220  
 659 His His Val Val Tyr Cys Phe Met Ile Ala Tyr Gly Thr Gln Arg Thr  
 660 225                    230                    235                    240  
 662 Leu Ile Leu Glu Ser Gln Asn Trp Arg Tyr Ala Thr Gly Gly Trp Glu  
 664                    245                    250                    255  
 666 Thr Val Phe Arg Pro Val Ser Glu Thr Cys Thr Asp Arg Ser Gly Ile  
 667                    260                    265                    270  
 669 Ser Thr Gly His Trp Ser Gly Glu Val Lys Asp Lys Asn Val Gln Val  
 670                    275                    280                    285

C2137

same end  
 in sequence 4  
 see p. 7



## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/575,096

DATE: 04/24/2006

TIME: 16:09:54

Input Set : A:\PTO.KD.txt

Output Set: N:\CRF4\04242006\J575096.raw

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673      290      295      300
675 Pro Leu Ala Val Pro Glu Asp Leu Ala Asp Arg Leu Val Arg Val His
676 305      310      315      320
678 Gly Asp Pro Ala Val Trp Trp Val Ser Gln Phe Val Lys Tyr Leu Ile
679      325      330      335
681 Arg Pro Gln Pro Trp Leu Glu Lys Glu Ile Glu Glu Ala Thr Lys Lys
682      340      345      350
684 Leu Gly Phe Lys His Pro Val Ile Gly Val His Val Arg Arg Thr Asp
685      355      360      365
687 Lys Val Gly Thr Glu Ala Ala Phe His Pro Ile Glu Glu Tyr Met Val
688      370      375      380
690 His Val Glu Glu His Phe Gln Leu Leu Ala Arg Arg Met Gln Val Asp
691 385      390      395      400
693 Lys Lys Arg Val Tyr Leu Ala Thr Asp Asp Pro Ser Leu Leu Lys Glu
694      405      410      415
696 Ala Lys Thr Lys Tyr Pro Asn Tyr Glu Phe Ile Ser Asp Asn Ser Ile
697      420      425      430
699 Ser Trp Ser Ala Gly Leu His Asn Arg Tyr Thr Glu Asn Ser Leu Arg
700      435      440      445
702 Gly Val Ile Leu Asp Ile His Phe Leu Ser Gln Ala Asp Phe Leu Val
703      450      455      460
705 Cys Thr Phe Ser Ser Gln Val Cys Arg Val Ala Tyr Glu Ile Met Gln
706 465      470      475      480
708 Thr Leu His Pro Asp Ala Ser Ala Asn Phe His Ser Leu Asp Asp Ile
709      485      490      495
711 Tyr Tyr Phe Gly Gly Gln Asn Ala His Asn Gln Ile Ala Ile Tyr Ala
712      500      505      510
714 His Gln Pro Arg Thr Ala Asp Glu Ile Pro Met Glu Pro Gly Asp Ile
715      515      520      525
717 Ile Gly Val Ala Gly Asn His Trp Asp Gly Tyr Ser Lys Gly Val Asn
718      530      535      540
720 Arg Lys Leu Gly Arg Thr Gly Leu Tyr Pro Ser Tyr Lys Val Arg Glu
721 545      550      555      560
723 Lys Ile Glu Thr Val Lys Tyr Pro Thr Tyr Pro Glu Ala Glu Lys
E--> 724      565      570

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5756-1212

10/575,096 8

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Met Trp Gln Leu Leu Leu Pro Thr Ala Leu Leu Leu

1 ± 5 - 10 -10

*misaligned numbers*

10/575,096 9

<400> 53

gaa ttc ggc atc atg tgg cag ctg ctc ctc cca act gct ctg cta ctt 48

Met Trp Gln Leu Leu Leu Pro Thr Ala Leu Leu Leu

7 7 5 5 10 10

*misaligned numbers*

<210> 54 *last sequence in file*  
 <211> 199  
 <212> PRT  
 <213> Homo sapiens

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 Gln Trp Tyr Arg Val Leu Glu Lys Asp Ser Val Thr Leu Lys Cys Gln  
 35 40 45  
 Gly Ala Tyr Ser Pro Glu Asp Asn Ser Thr Gln Trp Phe His Asn Glu  
 50 55 60  
 Ser Leu Ile Ser Ser Gln Ala Ser Ser Tyr Phe Ile Asp Ala Ala Thr  
 65 70 75 80  
 Val Asp Asp Ser Gly Glu Tyr Arg Cys Gln Thr Asn Leu Ser Thr Leu  
 85 90 95  
 Ser Asp Pro Val Gln Leu Glu Val His Ile Gly Trp Leu Leu Leu Gln  
 100 105 110  
 Ala Pro Arg Trp Val Phe Lys Glu Glu Asp Pro Ile His Leu Arg Cys  
 115 120 125  
 His Ser Trp Lys Asn Thr Ala Leu His Lys Val Thr Tyr Leu Gln Asn  
 130 135 140  
 Gly Lys Gly Arg Lys Tyr Phe His His Asn Ser Asp Phe Tyr Ile Pro  
 145 150 155 160  
 Lys Ala Thr Leu Lys Asp Ser Gly Ser Tyr Phe Cys Arg Gly Leu Phe  
 165 170 175  
 Gly Ser Lys Asn Val Ser Ser Glu Thr Val Asn Ile Thr Ile Thr Gln  
 180 185 190  
 Gly His His His His His His  
 195

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*delete*

**VERIFICATION SUMMARY**

**PATENT APPLICATION: US/10/575,096**

**DATE: 04/24/2006**

**TIME: 16:09:55**

**Input Set : A:\PTO.KD.txt**

**Output Set: N:\CRF4\04242006\J575096.raw**

L:10 M:270 C: Current Application Number differs, Replaced Current Application No  
 L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
 L:378 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:5  
 L:493 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:6  
 L:499 M:250 E: Invalid Numeric Identifier, INVALID IDENTIFIER  
 L:501 M:282 E: Numeric Field Identifier Missing, <213> is required.  
 L:608 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:7  
 L:614 M:250 E: Invalid Numeric Identifier, INVALID IDENTIFIER  
 L:616 M:282 E: Numeric Field Identifier Missing, <213> is required.  
 L:724 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:8  
 L:1044 M:283 W: Missing Blank Line separator, <220> field identifier  
 L:1045 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:1114 M:283 W: Missing Blank Line separator, <220> field identifier  
 L:1241 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:50  
 L:1244 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:50  
 L:1247 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:50  
 L:1250 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:50  
 L:1253 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:50  
 L:1256 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:50  
 L:1259 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:50  
 L:1262 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:50  
 L:1265 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:50  
 L:1268 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:50  
 L:1271 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:50  
 L:1274 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:50  
 L:1277 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:50  
 L:1280 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:50  
 L:1283 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:50  
 L:1355 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:53  
 L:1358 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:53  
 L:1361 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:53  
 L:1364 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:53  
 L:1367 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:53  
 L:1370 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:53  
 L:1373 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:53  
 L:1376 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:53  
 L:1379 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:53  
 L:1382 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:53  
 L:1385 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:53  
 L:1388 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:53  
 L:13 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (35) Counted  
 (54)